

SEQUENCE LISTING

<110> Sauter, Margret M.
Lorbiecke, Rene

<120> ALTERATION OF GROWTH AND ADAPTION UNDER HYPOXIC
CONDITIONS

<130> CropDesign

<140>

<141>

<160> 18

<170> PatentIn Ver. 2.1

<210> 1

<211> 872

<212> DNA

<213> Rice

<220>

<221> CDS

<222> (69)..(668)

<400> 1

```

agacgaacaa aaaacagaat ccatacgccat aatcgaaggt tcgctcttgc ttccacccccg 60
caatccac atg gag aac gaa ttc cag gat ggt aag acg gag gtg ata gaa 110
      Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu
        1              5              10

gca tgg tac atg gat gat agc gaa gag gac cag agg ctt cct cat cac 158
Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His
  15              20              25              30

cgc gaa ccc aaa gaa ttc att cct gtt gat aag ctt aca gaa cta gga 206
Arg Glu Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly
          35              40              45

gta atc agc tgg cgc cta aat cct gat aac tgg gag aat tgc gag aac 254
Val Ile Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn
          50              55              60

ctg aag aga atc cgc gaa gcc aga ggt tac tct tat gtg gac att tgt 302
Leu Lys Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys
          65              70              75

gat gtg tgc cca gag aag ctg cca aat tat gaa act aag atc aag agt 350
Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser
      80              85              90

```

0096739-105040

ttc ttt gaa gaa cac ctg cat acc gat gaa gaa ata cgc tat tgt ctt 398
 Phe Phe Glu Glu His Leu His Thr Asp Glu Glu Ile Arg Tyr Cys Leu
 95 100 105 110

 gaa ggg agt gga tac ttt gat gtg aga gac caa aat gat cag tgg att 446
 Glu Gly Ser Gly Tyr Phe Asp Val Arg Asp Gln Asn Asp Gln Trp Ile
 115 120 125

 cgt ata gca ctg aag aaa gga ggc atg att gtt ctg cct gca ggg atg 494
 Arg Ile Ala Leu Lys Lys Gly Gly Met Ile Val Leu Pro Ala Gly Met
 130 135 140

 tac cac cgc ttt acg ttg gac acc gac aac tat atc aag gca atg cga 542
 Tyr His Arg Phe Thr Leu Asp Thr Asp Asn Tyr Ile Lys Ala Met Arg
 145 150 155

 ctg ttt gtt ggc gat cct gtt tgg aca ccc tac aac cgt ccc cat gac 590
 Leu Phe Val Gly Asp Pro Val Trp Thr Pro Tyr Asn Arg Pro His Asp
 160 165 170

 cat ctt cct gca aga aag gag ttt ttg gct aaa ctt ctc aag tca gaa 638
 His Leu Pro Ala Arg Lys Glu Phe Leu Ala Lys Leu Leu Lys Ser Glu
 175 180 185 190

 ggt gaa aat caa gca gtt gaa ggc ttc tga gggttttgtt gggctcctgc 688
 Gly Glu Asn Gln Ala Val Glu Gly Phe
 195 200

 actgcgggttc tatattcaac ctgaataaga tgtgctatag caatgtaaat ttagcacagt 748
 ggctatggtc gccactcacc aacttgaagt gaaagattta atgatttttg ttaattctta 808
 tgtatcaatc ggcatatagc atttccgaaa tgtgtttttca ataaacagga gtcatagaagc 868
 tgaa 872

<210> 2
 <211> 199
 <212> PRT
 <213> Rice

<400> 2
 Met Glu Asn Glu Phe Gln Asp Gly Lys Thr Glu Val Ile Glu Ala Trp
 1 5 10 15
 Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu Pro His His Arg Glu
 20 25 30
 Pro Lys Glu Phe Ile Pro Val Asp Lys Leu Thr Glu Leu Gly Val Ile
 35 40 45
 Ser Trp Arg Leu Asn Pro Asp Asn Trp Glu Asn Cys Glu Asn Leu Lys
 50 55 60
 Arg Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Val Asp Ile Cys Asp Val
 65 70 75 80
 Cys Pro Glu Lys Leu Pro Asn Tyr Glu Thr Lys Ile Lys Ser Phe Phe
 85 90 95

```

<210> 3
<211> 980
<212> DNA
<213> Rice

<220>
<221> CDS
<222> (139)..(735)

<400> 3
cggacgcgtg ggcagattgc gttgagctga agctgttcgt gtgactcttc tacaccttcc 60
aggctatccg gaatcgggag ggtttcccaa taggaaagca actcaggact caggagcggc 120
gtctgagagg tttcagag atg gag aac cag ttc cag gat ggc aag gag gag 171
Met Glu Asn Gln Phe Gln Asp Gly Lys Glu Glu
1 5 10
gtc atc gaa gct tgg tac atg gat gac agt gaa gag gac cag agg ctt 219
Val Ile Glu Ala Trp Tyr Met Asp Asp Ser Glu Glu Asp Gln Arg Leu
15 20 25
cct cat cat cgt gag ccc aaa gaa ttc att cct ctt agc aaa ctt tca 267
Pro His His Arg Glu Pro Lys Glu Phe Ile Pro Leu Ser Lys Leu Ser
30 35 40
gag tta gga ata tta agc tgg cgc ctg aat gct gat gac tgg gag aat 315
Glu Leu Gly Ile Leu Ser Trp Arg Leu Asn Ala Asp Asp Trp Glu Asn
45 50 55
gat gag aac ctc aag aaa atc cgt gag gcc agg gga tac tct tac atg 363
Asp Glu Asn Leu Lys Lys Ile Arg Glu Ala Arg Gly Tyr Ser Tyr Met
60 65 70 75
gat att tgt gat gtg tgt cca gaa aag ctg cca aac tat gag gct aag 411
Asp Ile Cys Asp Val Cys Pro Glu Lys Leu Pro Asn Tyr Glu Ala Lys
80 85 90

```

<210>	4
<211>	198
<212>	PRT
<213>	Rice

<400> 4															
Met	Glu	Asn	Gln	Phe	Gln	Asp	Gly	Lys	Glu	Glu	Val	Ile	Glu	Ala	Trp
1				5					10					15	
Tyr	Met	Asp	Asp	Ser	Glu	Glu	Asp	Gln	Arg	Leu	Pro	His	His	Arg	Glu
			20					25					30		
Pro	Lys	Glu	Phe	Ile	Pro	Leu	Ser	Lys	Leu	Ser	Glu	Leu	Gly	Ile	Leu
		35					40					45			
Ser	Trp	Arg	Leu	Asn	Ala	Asp	Asp	Trp	Glu	Asn	Asp	Glu	Asn	Leu	Lys
	50					55					60				
Lys	Ile	Arg	Glu	Ala	Arg	Gly	Tyr	Ser	Tyr	Met	Asp	Ile	Cys	Asp	Val
65					70					75					80
Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Ala	Lys	Leu	Lys	Asn	Phe	Phe
				85					90					95	

Glu	Glu	His	Leu	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly
			100					105					110		
Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	Gln	Asn	Asp	Gln	Trp	Ile	Arg	Val
		115					120					125			
Ala	Val	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Met	Tyr	His
		130				135					140				
Arg	Phe	Thr	Leu	Asp	Ser	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe
145					150					155					160
Val	Gly	Glu	Pro	Val	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu
				165					170					175	
Pro	Ala	Arg	Lys	Glu	Tyr	Val	Glu	Lys	Ile	Ile	Asn	Arg	Gly	Gly	Thr
			180					185					190		
Gln	Ala	Val	Glu	Ala	Arg										
			195												

<210> 5
 <211> 774
 <212> DNA
 <213> Tomato

<220>
 <221> CDS
 <222> (1)..(591)

<400> 5																
gca	cca	gat	cca	aga	gag	gat	gtc	ata	cag	gca	tgg	tac	atg	gat	gac	48
Ala	Pro	Asp	Pro	Arg	Glu	Asp	Val	Ile	Gln	Ala	Trp	Tyr	Met	Asp	Asp	
1				5					10					15		
aac gat gag gac cag agg ctt cct cat cac cgt gag cca aag gaa ttt																96
Asn	Asp	Glu	Asp	Gln	Arg	Leu	Pro	His	His	Arg	Glu	Pro	Lys	Glu	Phe	
			20					25					30			
gtg tct ctt gac aag ctg gct gaa ctt gga gtg ctc agc tgg aga ctt																144
Val	Ser	Leu	Asp	Lys	Leu	Ala	Glu	Leu	Gly	Val	Leu	Ser	Trp	Arg	Leu	
		35					40					45				
gat gct gac aat tat gag act gat gag gag ttg aag aaa att cgg gaa																192
Asp	Ala	Asp	Asn	Tyr	Glu	Thr	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Glu	
	50					55					60					
gat cgt gga tat tca tac att gat ttc tgt gag gtt tgc cct gag aaa																240
Asp	Arg	Gly	Tyr	Ser	Tyr	Ile	Asp	Phe	Cys	Glu	Val	Cys	Pro	Glu	Lys	
	65				70				75					80		
cta ccg aat tac gag gag aaa atc aag aac ttt ttt gaa gaa cac ctg																288
Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Asn	Phe	Phe	Glu	Glu	His	Leu	
				85				90					95			
cac acc gac gag gag atc cgt tac gct gtt gca gga agt ggt tac ttt																336
His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Ala	Val	Ala	Gly	Ser	Gly	Tyr	Phe	
			100					105					110			

009799-021601

gat gtc cgc gat gtg aat gag agc tgg att cgc gtc tgg gta aag aaa 384
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125

ggt gga atg att gtt ctt cct gct gga atc tat cac cgc ttc acg ctt 432
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

gat tca agc aac tac att aag gca atg cgt ctc ttt gtt ggt gac cca 480
Asp Ser Ser Asn Tyr Ile Lys Ala Met Arg Leu Phe Val Gly Asp Pro
145 150 155 160

att tgg act cca tac aat cgt cca cat gat cat ctt ccc gca agg caa 528
Ile Trp Thr Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Gln
165 170 175

gaa tat gtt gag acg ttt gtc aac gca gat ggc gct ggt cgt gct gtt 576
Glu Tyr Val Glu Thr Phe Val Asn Ala Asp Gly Ala Gly Arg Ala Val
180 185 190

aat gct gct gct taa atcaactata ggagaggaat ttgaaatcgt actagattgt 631
Asn Ala Ala Ala
195

aataaatatt accatatggt ggcttttgctg ttctttgatgt gtgccttact aagcatgttt 691

aatgttgtat tgtggcacta aataaatcac cccctatggg agattgattg tttatatgca 751

agtggaattt attatgtgat ttt 774

<210> 6
<211> 196
<212> PRT
<213> Tomato

<400> 6
Ala Pro Asp Pro Arg Glu Asp Val Ile Gln Ala Trp Tyr Met Asp Asp
1 5 10 15
Asn Asp Glu Asp Gln Arg Leu Pro His His Arg Glu Pro Lys Glu Phe
20 25 30
Val Ser Leu Asp Lys Leu Ala Glu Leu Gly Val Leu Ser Trp Arg Leu
35 40 45
Asp Ala Asp Asn Tyr Glu Thr Asp Glu Glu Leu Lys Lys Ile Arg Glu
50 55 60
Asp Arg Gly Tyr Ser Tyr Ile Asp Phe Cys Glu Val Cys Pro Glu Lys
65 70 75 80
Leu Pro Asn Tyr Glu Glu Lys Ile Lys Asn Phe Phe Glu Glu His Leu
85 90 95
His Thr Asp Glu Glu Ile Arg Tyr Ala Val Ala Gly Ser Gly Tyr Phe
100 105 110
Asp Val Arg Asp Val Asn Glu Ser Trp Ile Arg Val Trp Val Lys Lys
115 120 125
Gly Gly Met Ile Val Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu
130 135 140

007593-0064

```
<210> 7
<211> 603
<212> DNA
<213> Tomato

<220>
<221> CDS
<222> (3)..(572)
```

<400> 7																
aa	atg	gca	atc	gag	tgt	aag	gca	tgg	ttt	atg	gat	gaa	aat	tca	gaa	47
	Met	Ala	Ile	Glu	Cys	Lys	Ala	Trp	Phe	Met	Asp	Glu	Asn	Ser	Glu	
	1				5					10					15	
gat	cag	cgg	cta	ccg	cac	cag	aag	aac	cca	ccg	gag	ttt	gtt	tca	gtg	95
Asp	Gln	Arg	Leu	Pro	His	Gln	Lys	Asn	Pro	Pro	Glu	Phe	Val	Ser	Val	
				20					25					30		
gag	aaa	tta	gca	gta	atc	gga	gtt	tta	tac	tgg	aaa	ttg	aac	cct	aat	143
Glu	Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn	
			35					40					45			
gat	tac	gag	aac	gat	gaa	gaa	ttg	aaa	aaa	att	cgt	caa	agt	aga	ggc	191
Asp	Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Gln	Ser	Arg	Gly	
		50					55					60				
tac	agc	tac	atg	gac	ttg	ctg	gat	ttg	tgc	cct	gag	aag	gtg	gat	aac	239
Tyr	Ser	Tyr	Met	Asp	Leu	Leu	Asp	Leu	Cys	Pro	Glu	Lys	Val	Asp	Asn	
	65				70						75					
tat	gag	cag	aag	ttg	aaa	aat	ttc	tat	acg	gag	cac	ata	cac	gca	gat	287
Tyr	Glu	Gln	Lys	Leu	Lys	Asn	Phe	Tyr	Thr	Glu	His	Ile	His	Ala	Asp	
	80				85					90					95	
gag	gag	ata	cgt	tac	tgt	ctg	gaa	ggg	agt	gga	tat	ttt	gat	gtg	aga	335
Glu	Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	
				100					105					110		
gac	aag	gat	gat	cgc	tgg	att	cgc	atc	tgg	atg	aag	gcc	ggt	gat	atg	383
Asp	Lys	Asp	Asp	Arg	Trp	Ile	Arg	Ile	Trp	Met	Lys	Ala	Gly	Asp	Met	
			115					120					125			
att	gtc	ttg	cct	gct	ggg	att	tac	cac	cgg	ttc	acc	cta	gat	act	gat	431
Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	
		130					135					140				

aac	tat	gtc	aag	ttg	atg	agg	ttg	ttt	gtg	gga	gag	ccg	gtg	tgg	acg	479
Asn	Tyr	Val	Lys	Leu	Met	Arg	Leu	Phe	Val	Gly	Glu	Pro	Val	Trp	Thr	
145						150					155					
cct	tac	aat	cga	cca	caa	gaa	gat	cat	cca	gca	agg	aag	gag	tac	atc	527
Pro	Tyr	Asn	Arg	Pro	Gln	Glu	Asp	His	Pro	Ala	Arg	Lys	Glu	Tyr	Ile	
160					165					170					175	
aag	agt	gtt	act	gaa	aga	gta	gga	gtg	cct	ctt	aca	gca	cac	taa		572
Lys	Ser	Val	Thr	Glu	Arg	Val	Gly	Val	Pro	Leu	Thr	Ala	His			
				180					185					190		
gacatatatttg agctttacaa acctgagagt g															603	

<210> 8
 <211> 189
 <212> PRT
 <213> Tomato

<400> 8																
Met	Ala	Ile	Glu	Cys	Lys	Ala	Trp	Phe	Met	Asp	Glu	Asn	Ser	Glu	Asp	
1				5					10					15		
Gln	Arg	Leu	Pro	His	Gln	Lys	Asn	Pro	Pro	Glu	Phe	Val	Ser	Val	Glu	
		20					25						30			
Lys	Leu	Ala	Val	Ile	Gly	Val	Leu	Tyr	Trp	Lys	Leu	Asn	Pro	Asn	Asp	
	35						40					45				
Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Gln	Ser	Arg	Gly	Tyr	
	50					55					60					
Ser	Tyr	Met	Asp	Leu	Leu	Asp	Leu	Cys	Pro	Glu	Lys	Val	Asp	Asn	Tyr	
65				70					75					80		
Glu	Gln	Lys	Leu	Lys	Asn	Phe	Tyr	Thr	Glu	His	Ile	His	Ala	Asp	Glu	
			85						90					95		
Glu	Ile	Arg	Tyr	Cys	Leu	Glu	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	
		100						105					110			
Lys	Asp	Asp	Arg	Trp	Ile	Arg	Ile	Trp	Met	Lys	Ala	Gly	Asp	Met	Ile	
	115						120					125				
Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	
	130					135					140					
Tyr	Val	Lys	Leu	Met	Arg	Leu	Phe	Val	Gly	Glu	Pro	Val	Trp	Thr	Pro	
145					150					155					160	
Tyr	Asn	Arg	Pro	Gln	Glu	Asp	His	Pro	Ala	Arg	Lys	Glu	Tyr	Ile	Lys	
			165						170					175		
Ser	Val	Thr	Glu	Arg	Val	Gly	Val	Pro	Leu	Thr	Ala	His				
			180					185								

0028E23-0450
 105700-00250250


```
<220>  
<221> CDS  
<222> (32) .. (634)
```

cgaacccgtc gtagcagaaa aacttggtcac c atg gtt tct tcc gac aag gat 52
Met Val Ser Ser Asp Lys Asp
1 5

cca cga gag gat gtc ctt caa gcc tgg tac atg gat gat agt gat gaa 100
Pro Arg Glu Asp Val Leu Gln Ala Trp Tyr Met Asp Asp Ser Asp Glu
10 15 20

gat	caa	aga	ctc	ccc	cac	cac	aaa	gaa	ccc	aag	gag	ttt	gtc	tcg	ttg	148
Asp	Gln	Arg	Leu	Pro	His	His	Lys	Glu	Pro	Lys	Glu	Phe	Val	Ser	Leu	
	25					30					35					

gac caa ctt gct gaa ctt gga gtc ctt agc tgg aaa cta gat gct gat 196
Asp Gln Leu Ala Glu Leu Gly Val Leu Ser Trp Lys Leu Asp Ala Asp
40 45 50 55

aac cat gaa aat gat cca gag ctg aag aag att cgt gaa gag cgt ggt 244
Asn His Glu Asn Asp Pro Glu Leu Lys Lys Ile Arg Glu Glu Arg Gly
60 65 70

tac	acc	tac	atg	gat	gtt	tgt	gag	gtc	tgc	cca	gaa	aag	ttg	cca	aat	292
Tyr	Thr	Tyr	Met	Asp	Val	Cys	Glu	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn	
			75					80					85			

tat	gaa	cag	aaa	atc	aaa	agc	ttc	ttt	gaa	gag	cat	ctt	cac	act	gat	340
Tyr	Glu	Gln	Lys	Ile	Lys	Ser	Phe	Phe	Glu	Glu	His	Leu	His	Thr	Asp	
		90					95					100				

gag gag atc cgc ttt tgt gct gct gga agt ggc tat ttt gat gtt agg 388
Glu Glu Ile Arg Phe Cys Ala Ala Gly Ser Gly Tyr Phe Asp Val Arg
105 110 115

gat cgc aat gaa gct tgg att cgt gtg tgg gtc aag aaa gga gga atg 436
Asp Arg Asn Glu Ala Trp Ile Arg Val Trp Val Lys Lys Gly Gly Met
120 125 130 135

atc	atc	tta	cct	gcc	gga	att	tat	cat	cgc	ttt	acg	cta	gat	gag	agc	484
Ile	Ile	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Glu	Ser	
				140					145					150		

aac tac att aag gct ttg cgt ttt ttt gtt ggt gag cca gtt tgg act 532
Asn Tyr Ile Lys Ala Leu Arg Phe Phe Val Gly Glu Pro Val Trp Thr
155 160 165

[illegible]

<210>	11
<211>	933
<212>	DNA
<213>	Cotton

```
<220>
<221> CDS
<222> (33) .. (635)
```

<div> <div><400> 11</div> <div> <div>atattttttttt</div> <div>aatttgacg</div> <div>g</div> <div>aaaaaaaaa</div> <div>ct</div> <div>atg</div> <div>acc</div> <div>atg</div> <div>ggt</div> <div>tct</div> <div>gca</div> <div>gac</div> <div>53</div> </div> </div>																
<div> <div>Met</div> <div>Thr</div> <div>Met</div> <div>Gly</div> <div>Ser</div> <div>Ala</div> <div>Asp</div> <div>1</div> <div>5</div> </div>																
aag	agg	gag	gaa	gtt	att	cag	gca	tgg	tac	atg	gat	gat	agt	gat	gaa	101
Lys	Arg	Glu	Glu	Val	Ile	Gln	Ala	Trp	Tyr	Met	Asp	Asp	Ser	Asp	Glu	
<div> <div>10</div> <div>15</div> <div>20</div> </div>																
gat	cag	agg	ctt	cct	cat	cac	cgt	gaa	cct	aag	gaa	tat	gta	tcc	ttg	149
Asp	Gln	Arg	Leu	Pro	His	His	Arg	Glu	Pro	Lys	Glu	Tyr	Val	Ser	Leu	
<div> <div>25</div> <div>30</div> <div>35</div> </div>																
gat	aaa	ctt	gct	gag	ctt	gga	gta	ctc	agc	tgg	cga	ttg	gat	gct	gat	197
Asp	Lys	Leu	Ala	Glu	Leu	Gly	Val	Leu	Ser	Trp	Arg	Leu	Asp	Ala	Asp	
<div> <div>40</div> <div>45</div> <div>50</div> <div>55</div> </div>																
aac	tat	gaa	aat	gat	gaa	gag	ttg	aag	aaa	att	cgt	gaa	gaa	cga	ggg	245
Asn	Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys	Lys	Ile	Arg	Glu	Glu	Arg	Gly	
<div> <div>60</div> <div>65</div> <div>70</div> </div>																
tac	tcc	tac	atg	gac	ttc	tgc	gag	gtt	tgc	cct	gag	aag	ctt	cca	aat	293
Tyr	Ser	Tyr	Met	Asp	Phe	Cys	Glu	Val	Cys	Pro	Glu	Lys	Leu	Pro	Asn	
<div> <div>75</div> <div>80</div> <div>85</div> </div>																
tat	gag	gag	aag	ata	aaa	aat	ttc	ttc	gaa	gaa	cat	att	cat	act	gat	341
Tyr	Glu	Glu	Lys	Ile	Lys	Asn	Phe	Phe	Glu	Glu	His	Ile	His	Thr	Asp	
<div> <div>90</div> <div>95</div> <div>100</div> </div>																
gag	gag	atc	cgt	tac	tgt	gtg	gca	gga	agt	ggg	tat	ttt	gat	gta	cgg	389
Glu	Glu	Ile	Arg	Tyr	Cys	Val	Ala	Gly	Ser	Gly	Tyr	Phe	Asp	Val	Arg	
<div> <div>105</div> <div>110</div> <div>115</div> </div>																
gat	cat	aat	gat	aaa	tgg	att	cgt	gtg	tgg	gtg	aag	aaa	gga	ggc	atg	437
Asp	His	Asn	Asp	Lys	Trp	Ile	Arg	Val	Trp	Val	Lys	Lys	Gly	Gly	Met	
<div> <div>120</div> <div>125</div> <div>130</div> <div>135</div> </div>																
ata	gtt	tta	cct	gct	gga	att	tat	cat	cgc	ttt	act	ctg	gat	aca	gac	485
Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	Leu	Asp	Thr	Asp	
<div> <div>140</div> <div>145</div> <div>150</div> </div>																
aac	tat	att	aag	gca	atg	cgg	ctc	ttt	gtt	ggg	gat	cca	att	tgg	act	533
Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Asp	Pro	Ile	Trp	Thr	
<div> <div>155</div> <div>160</div> <div>165</div> </div>																

ccg tac aat cgt ccg cac gat cat ctt cct gca agg aag gag tat atc 581
Pro Tyr Asn Arg Pro His Asp His Leu Pro Ala Arg Lys Glu Tyr Ile
170 175 180

aag aac ttt ttg cgg gag gaa ggt ggt ggc caa gcc gtt gat gct gcc 629
Lys Asn Phe Leu Arg Glu Glu Gly Gly Gly Gln Ala Val Asp Ala Ala
185 190 195

gca taa aatcaacatt catctggtgg tggccaagtc gttgatgctg ccgcataaaa 685
Ala
200

tcagcattca tctctggtat cgtgtcttat aaaatatgaa accccggatt tgtggtaata 745

aataagtcta ggcttgtctg cttttgatgc gtggatatgg atcgttatgg ttgttgcttg 805

ctatatattg cctattccat atcgaaaatt cgcaaacttg ctatgtattt ctacatttta 865

tgtgcttact accagattgg ctcttaataa tcaaagttaa cataatatac atttcgtcga 925

cgcgggccg 933

<210> 12

<211> 200

<212> PRT

<213> Cotton

<400> 12

Met	Thr	Met	Gly	Ser	Ala	Asp	Lys	Arg	Glu	Glu	Val	Ile	Gln	Ala	Trp
1				5					10					15	
Tyr	Met	Asp	Asp	Ser	Asp	Glu	Asp	Gln	Arg	Leu	Pro	His	His	Arg	Glu
		20						25					30		
Pro	Lys	Glu	Tyr	Val	Ser	Leu	Asp	Lys	Leu	Ala	Glu	Leu	Gly	Val	Leu
		35					40					45			
Ser	Trp	Arg	Leu	Asp	Ala	Asp	Asn	Tyr	Glu	Asn	Asp	Glu	Glu	Leu	Lys
	50					55					60				
Lys	Ile	Arg	Glu	Glu	Arg	Gly	Tyr	Ser	Tyr	Met	Asp	Phe	Cys	Glu	Val
	65				70				75					80	
Cys	Pro	Glu	Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Asn	Phe	Phe
				85					90					95	
Glu	Glu	His	Ile	His	Thr	Asp	Glu	Glu	Ile	Arg	Tyr	Cys	Val	Ala	Gly
			100					105					110		
Ser	Gly	Tyr	Phe	Asp	Val	Arg	Asp	His	Asn	Asp	Lys	Trp	Ile	Arg	Val
		115					120					125			
Trp	Val	Lys	Lys	Gly	Gly	Met	Ile	Val	Leu	Pro	Ala	Gly	Ile	Tyr	His
	130					135					140				
Arg	Phe	Thr	Leu	Asp	Thr	Asp	Asn	Tyr	Ile	Lys	Ala	Met	Arg	Leu	Phe
	145				150					155				160	
Val	Gly	Asp	Pro	Ile	Trp	Thr	Pro	Tyr	Asn	Arg	Pro	His	Asp	His	Leu
				165					170					175	
Pro	Ala	Arg	Lys	Glu	Tyr	Ile	Lys	Asn	Phe	Leu	Arg	Glu	Glu	Gly	Gly
			180					185					190		
Gly	Gln	Ala	Val	Asp	Ala	Ala	Ala								
		195					200								

<210> 13
 <211> 919
 <212> DNA
 <213> Human

<220>
 <221> CDS
 <222> (1)..(564)

<400> 13

cga	aca	cgg	cac	ccg	cac	tgc	gcg	tca	gtg	gtg	cag	gcc	tgg	tat	atg	48
Arg	Thr	Arg	His	Pro	His	Cys	Ala	Ser	Val	Val	Gln	Ala	Trp	Tyr	Met	
1				5					10					15		
gac	gac	gcc	ccg	ggc	acc	cgc	ggc	aac	ccc	acc	gcc	ccg	acc	ccg	gcc	96
Asp	Asp	Ala	Pro	Gly	Thr	Arg	Gly	Asn	Pro	Thr	Ala	Pro	Thr	Pro	Ala	
			20					25					30			
gcc	cag	tgc	gct	gga	gca	gct	gcg	cgg	ctc	ggg	gtg	ctc	tac	tgg	aag	144
Ala	Gln	Cys	Ala	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Val	Leu	Tyr	Trp	Lys	
		35					40					45				
ctg	gat	gct	gac	aaa	tat	gag	aat	gat	cca	gaa	tta	gaa	aag	atc	cga	192
Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys	Ile	Arg	
	50					55					60					
aga	gag	agg	aac	tac	tcc	tgg	atg	gac	atc	ata	acc	ata	tgc	aaa	gat	240
Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys	Lys	Asp	
65					70					75					80	
aaa	cta	cca	aat	tat	gaa	gaa	aag	att	aag	atg	ttc	tac	gag	gag	cat	288
Lys	Leu	Pro	Asn	Tyr	Glu	Glu	Lys	Ile	Lys	Met	Phe	Tyr	Glu	Glu	His	
			85						90					95		
ttg	cac	ttg	gac	gat	gag	atc	cgc	tac	atc	ctg	gat	ggc	agt	ggg	tac	336
Leu	His	Leu	Asp	Asp	Glu	Ile	Arg	Tyr	Ile	Leu	Asp	Gly	Ser	Gly	Tyr	
			100					105					110			
ttc	gat	gtg	agg	gac	aag	gag	gac	cag	tgg	atc	cgg	atc	ttc	atg	gag	384
Phe	Asp	Val	Arg	Asp	Lys	Glu	Asp	Gln	Trp	Ile	Arg	Ile	Phe	Met	Glu	
		115					120					125				
aag	gga	gac	atg	gtg	acg	ctc	ccc	gcg	ggg	atc	tat	cac	cgc	ttc	acg	432
Lys	Gly	Asp	Met	Val	Thr	Leu	Pro	Ala	Gly	Ile	Tyr	His	Arg	Phe	Thr	
	130					135					140					
gtg	gac	gag	aag	aac	tac	acg	aag	gcc	atg	cgg	ctg	ttt	gtg	gga	gaa	480
Val	Asp	Glu	Lys	Asn	Tyr	Thr	Lys	Ala	Met	Arg	Leu	Phe	Val	Gly	Glu	
145					150					155					160	
ccg	gtg	tgg	aca	gcg	tac	aac	cgg	ccc	gct	gac	cat	ttt	gaa	gcc	cgc	528
Pro	Val	Trp	Thr	Ala	Tyr	Asn	Arg	Pro	Ala	Asp	His	Phe	Glu	Ala	Arg	
				165					170					175		

ggg cag tac gtg aaa ttt ctg gca cag acc gcc tag cagtgcctgcc 574
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

tgggaactaa cacgtgcctc gtaaaggctcc ccaatgtaat gaactgagca gaaaattcaa 634
tcaactttct ctttgctttt agaggatagc cttgaggtag attatctttc ctttgtaaga 694
ttatttgatc agaataatttt gtaatgaaag gatctagaaa gcaacttgga agtgtaaaga 754
gtcaccttca ttttctgtaa ctcaatcaag actgggtgggt ccatggccct gtgttagttc 814
attgcattca ggttgagtcc caaatgaaag tttcatctcc cgaaatgcag ttccttagat 874
gcccactctgg acgtgaatgc cgcgcctgcg tgtaagaagg tgcaat 920

<210> 14
<211> 187
<212> PRT
<213> Human

<400> 14
Arg Thr Arg His Pro His Cys Ala Ser Val Val Gln Ala Trp Tyr Met
1 5 10 15
Asp Asp Ala Pro Gly Thr Arg Gly Asn Pro Thr Ala Pro Thr Pro Ala
20 25 30
Ala Gln Cys Ala Gly Ala Ala Ala Arg Leu Gly Val Leu Tyr Trp Lys
35 40 45
Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg
50 55 60
Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp
65 70 75 80
Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His
85 90 95
Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr
100 105 110
Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu
115 120 125
Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr
130 135 140
Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu
145 150 155 160
Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg
165 170 175
Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
180 185

<210> 15
 <211> 972
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (17)..(556)

<400> 15
 agccgccgcc gccacc atg gtg cag gcc tgg tat atg gac gag tcc acc gcc 52
 Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr Ala
 1 5 10

gac ccg cgg aag ccc cac cgc gca cag ccc gac cgc ccc gtg agc ctg 100
 Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser Leu
 15 20 25

gag cag ctg cgc acg ctc gga gtg ctc tat tgg aag cta gat gct gac 148
 Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala Asp
 30 35 40

aag tat gag aac gat cca gaa cta gaa aag atc cgg aaa atg aga aac 196
 Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg Asn
 45 50 55 60

tac tcc tgg atg gac atc atc acc ata tgc aaa gat aca ctt ccc aat 244
 Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro Asn
 65 70 75

tac gag gag aag atc aag atg ttc ttt gag gaa cat ctg cat ctg gat 292
 Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu Asp
 80 85 90

gag gag atc cgc tac atc ctg gag ggt agt ggg tac ttc gat gtc agg 340
 Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val Arg
 95 100 105

gac aag gag gac aag tgg atc cgg att tcc atg gag aag ggg gac atg 388
 Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp Met
 110 115 120

att act ctt cct gcc ggc atc tat cac cgc ttc aca ctg gac gag aag 436
 Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu Lys
 125 130 135 140

aat tac gtg aag gcc atg cgg ctg ttt gtt gga gaa cct gtg tgg aca 484
 Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Thr
 145 150 155

cca tac aac cgg cca gct gac cat ttt gat gcc cgt gta cag tac atg 532
 Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr Met
 160 165 170

agt ttt ttg gaa gga aca gca tag cagtgtcct caaagagaaa actgcactgt 586
 Ser Phe Leu Glu Gly Thr Ala
 175 180

gtgaatctcc tgctgtggta accgaatgga aagttgtctca cttttctgct tttgtatttg 646
 aacttgaggg tagactagct ctcttttgcta ggattgtgag atcagtgtct tttaaatgaa 706
 agcctctcta aaagtgagtt ttacatggaa gccacaaaaa tgtgaaaaag tgaccttaat 766
 tttccctaac tgtcaagact tagaggtata ggagccctgg attggtatgt gcattcatgc 826
 atggccaatc ttcattctccc agatcttttag gtgtctgttg gtgtgaagct atgcctcctg 886
 caagaggggca gttataacca gcacaactaa ccagatgacg tttttctcct ttgctgattg 946
 ttgagtgggg aagtgggggtt gttgtt 972

<210> 16
 <211> 179
 <212> PRT
 <213> Mouse

<400> 16
 Ala Ala Ala Ala Thr Met Val Gln Ala Trp Tyr Met Asp Glu Ser Thr
 1 5 10 15
 Ala Asp Pro Arg Lys Pro His Arg Ala Gln Pro Asp Arg Pro Val Ser
 20 25 30
 Leu Glu Gln Leu Arg Thr Leu Gly Val Leu Tyr Trp Lys Leu Asp Ala
 35 40 45
 Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Lys Met Arg
 50 55 60
 Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Thr Leu Pro
 65 70 75 80
 Asn Tyr Glu Glu Lys Ile Lys Met Phe Phe Glu Glu His Leu His Leu
 85 90 95
 Asp Glu Glu Ile Arg Tyr Ile Leu Glu Gly Ser Gly Tyr Phe Asp Val
 100 105 110
 Arg Asp Lys Glu Asp Lys Trp Ile Arg Ile Ser Met Glu Lys Gly Asp
 115 120 125
 Met Ile Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Leu Asp Glu
 130 135 140
 Lys Asn Tyr Val Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp
 145 150 155 160
 Thr Pro Tyr Asn Arg Pro Ala Asp His Phe Asp Ala Arg Val Gln Tyr
 165 170 175
 Met Ser Phe Leu Glu Gly Thr Ala
 180

<210> 17
 <211> 706
 <212> DNA
 <213> Zebrafish

<220>
 <221> CDS
 <222> (36)..(581)

<400> 17

```

gtactgcgca tggagaccga accggactgt tcaag atg agt gtt ttc gag gca      53
                Met Ser Val Phe Glu Ala
                        1                      5

tgg tac atg gat gaa gag tcc gga gag gac cag aga ctc ccg cac aaa      101
Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp Gln Arg Leu Pro His Lys
                10                      15                      20

ctg agc ccg aat cag ccc gtc agc gtc cag cag ctg gag cac atc gga      149
Leu Ser Pro Asn Gln Pro Val Ser Val Gln Gln Leu Glu His Ile Gly
                25                      30                      35

gtc ttt cac tgg aag ctg aac gct gat atc tat gaa aat gac ccc gaa      197
Val Phe His Trp Lys Leu Asn Ala Asp Ile Tyr Glu Asn Asp Pro Glu
                40                      45                      50

ctg cag aag atc cga gag gag aag ggt tat tcc ttt atg gac atc ata      245
Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr Ser Phe Met Asp Ile Ile
                55                      60                      65                      70

acc att cac ccg gac aaa ctg ccc gat tac caa aac aaa ctg aaa atg      293
Thr Ile His Pro Asp Lys Leu Pro Asp Tyr Gln Asn Lys Leu Lys Met
                75                      80                      85

ttt tac gaa gag cat ctc cac ctg gac gat gag atc cgt tat att ctg      341
Phe Tyr Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu
                90                      95                      100

gaa gga tcc tct tat ttt gat gtg cgg gac gaa ggc gac cgc tgg atc      389
Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp Glu Gly Asp Arg Trp Ile
                105                      110                      115

cga ata gcg gtg tct aaa ggc gac ctc atc act tta ccg gcc ggg att      437
Arg Ile Ala Val Ser Lys Gly Asp Leu Ile Thr Leu Pro Ala Gly Ile
                120                      125                      130

tac cac aga ttc acc gtg gac gaa agc aac tac act aaa gcc atg cgt      485
Tyr His Arg Phe Thr Val Asp Glu Ser Asn Tyr Thr Lys Ala Met Arg
                135                      140                      145                      150

ctg ttc gtg ggt gaa ccc gtc tgg aag gcc tac aac cgt cca gcc gat      533
Leu Phe Val Gly Glu Pro Val Trp Lys Ala Tyr Asn Arg Pro Ala Asp
                155                      160                      165

```

gac ttt gac atc cgc aag gaa tac gtg aac tcg ctg gga agc tcc tga 581
 Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn Ser Leu Gly Ser Ser
 170 175 180

aatgcctgat gggattgatt tagtgctgag aatcagactc tgcggtgcct tanacagaca 641
 ngcagcaata gtagagctaa catgtcatta cttagtcatc aagacacacc tgatataaag 701
 attat 706

<210> 18
 <211> 181
 <212> PRT
 <213> Zebrafish

<400> 18
 Met Ser Val Phe Glu Ala Trp Tyr Met Asp Glu Glu Ser Gly Glu Asp
 1 5 10 15
 Gln Arg Leu Pro His Lys Leu Ser Pro Asn Gln Pro Val Ser Val Gln
 20 25 30
 Gln Leu Glu His Ile Gly Val Phe His Trp Lys Leu Asn Ala Asp Ile
 35 40 45
 Tyr Glu Asn Asp Pro Glu Leu Gln Lys Ile Arg Glu Glu Lys Gly Tyr
 50 55 60
 Ser Phe Met Asp Ile Ile Thr Ile His Pro Asp Lys Leu Pro Asp Tyr
 65 70 75 80
 Gln Asn Lys Leu Lys Met Phe Tyr Glu Glu His Leu His Leu Asp Asp
 85 90 95
 Glu Ile Arg Tyr Ile Leu Glu Gly Ser Ser Tyr Phe Asp Val Arg Asp
 100 105 110
 Glu Gly Asp Arg Trp Ile Arg Ile Ala Val Ser Lys Gly Asp Leu Ile
 115 120 125
 Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp Glu Ser Asn
 130 135 140
 Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val Trp Lys Ala
 145 150 155 160
 Tyr Asn Arg Pro Ala Asp Asp Phe Asp Ile Arg Lys Glu Tyr Val Asn
 165 170 175
 Ser Leu Gly Ser Ser
 180